





Genforce version 4.5  
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OM protein protein search, using sw model

Run on: August 30, 2001, 16:21:02 : Search time 10.04 seconds

without alignments)

34.119 million cell updates/sec

US-09-018-194-9

57

1 GATDIKGAEC 10

Scoring table:

Gapop 10.0 , Gapext 0.5

93435 seqs, 34255486 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description
1	48	66.7	362	1	MOM2_CAEEL	Q10459 caenorhabdi
2	48	66.7	963	1	UBP4_HUMAN	Q14107 homo sapien
3	48	66.7	2703	1	NOPC_OBOMF	P07207 drosophila
4	35	61.4	118	1	PA21_LATSE	P00611 latitanda s
5	35	61.4	118	1	PA23_LATSE	P00612 latitanda s
6	35	61.4	118	1	PA24_LATSE	P00613 latitanda s
7	35	61.4	119	1	PA21_OXYSC	P00614 xenopus lae
8	35	61.4	404	1	PRSB_XENLA	O42586 xenopus lae
9	35	61.4	439	1	PRSA_HUMAN	P17980 homo sapien
10	35	61.4	439	1	PRSA_RAT	O63569 rattus norv
11	35	61.4	1124	1	TIF2_HUMAN	Q02763 homo sapien
12	35	61.4	1125	1	TIF2_HUMAN	Q06807 homo sapien
13	34	59.6	229	1	NKF_PIG	Q29074 sus scrofa
14	34	59.6	231	1	NKF_GOVIN	P14600 bos taurus
15	34	59.6	241	1	NKF_XENLA	P21617 xenopus lae
16	34	59.6	241	1	NKF_CAVPO	P19094 cavia porco
17	34	59.6	241	1	NKF_HUMAN	P01148 homo sapien
18	34	59.6	241	1	NKF_MOUSE	P01139 mus musculu
19	34	59.6	241	1	NKF_RAT	P25427 rattus norv
20	34	59.6	243	1	NKF_CHICK	P05200 gallus gall
21	34	59.6	254	1	ASFG_YEAST	P40403 saccharomyc
22	34	59.6	322	1	ASFG_BACLI	P30463 bacillus li
23	34	59.6	379	1	P2X6_MOUSE	O54803 mus musculu
24	34	59.6	379	1	P2X6_RAT	P51579 rattus norv
25	34	59.6	534	1	U013_HUMAN	P35503 homo sapien
26	34	59.6	534	1	U015_HUMAN	P22410 homo sapien
27	34	59.6	534	1	U015_HUMAN	P35504 homo sapien
28	34	59.6	81	1	Y061_HUMAN	O54608 halobacteri
29	34	59.6	106	1	CV2_BROGL	P00009 rhodospilla 9
30	34	59.6	129	1	RS11_METJA	P54021 metthanoce
31	34	59.6	151	1	Y447_METJA	O57794 metthanoce
32	34	59.6	196	1	HL1J_ECOLI	O46948 escherichia
33	34	59.6	208	1	RL13_SCHPO	O74175 schizosacch

34	33	57.9	241	1	NCF_FRANA	P06775 pseudots
35	33	57.9	279	1	ESR2_HUMAN	Q04705 mouse
36	33	57.9	365	1	AROC_HUMAN	Q05711 human
37	33	57.9	530	1	ESR2_CALJA	Q05711 human
38	33	57.9	530	1	ESR2_HUMAN	Q05711 human
39	33	57.9	824	1	CV22_HUMAN	Q05711 human
40	33	57.9	962	1	UBP4_MOUSE	P00611 latitanda s
41	33	57.9	1088	1	Y054_YEAST	P00611 latitanda s
42	33	57.9	1134	1	Y054_YEAST	P00611 latitanda s
43	33	57.9	2437	1	NCF_MOUSE	Q04705 mouse
44	32	56.1	117	1	PA2A_PSEBO	P25258 pseudots
45	32	56.1	117	1	PA2B_PSEBO	P25258 pseudots

## ALIGNMENTS

RESULT	1
MOM2_CAEEL	
ID	MOM2_CAEEL
AI	Q10459; 016146; PRT; 362 AA.
DI	01-OCT-2000 (rel. 40, Created)
DI	01-OCT-2000 (rel. 40, Last sequence update)
DI	01-OCT-2000 (rel. 40, Last annotation update)
DE	MOM-2 PROTEIN PRECURSOR.
GN	MOM-2 OR F38E1.7.
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae.
OC	Rhabditidae; Telodermata; Caenorhabditis.
OX	NCHI_TaxID:6249;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN BRISTOL N2;
RX	MEYER, R.E. 1974; PUBMED 2285750;
KA	Rochelleau C.E., Towns W.D., Lin K., Wiltmann C., Reilly V., Ha.
KA	Alti M., Priss J.R., Mello C.C.
RT	"Wnt signaling and an APC-related gene specify endoderm in early C.
RI	elephant embryos."
RL	Cell 90:707-716(1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN-BRISTOL N2;
KA	Galland S., Le T.
RT	Submitted (1997) to the EMBL, GenBank, DDBJ databases.
CC	1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN INVOLVED IN ENDOERM
CC	SPECIFICATION AND CLEAVAGE AXIS DETERMINATION.
CC	1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC	EXTRACELLULAR MATRIX.
CC	1- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC	enterprises requires a license agreement. Please contact EMBL or send an email to license@isb.sib.ch).
CC	EMBL: AF013952; AAC47749.1;
DR	EMBL: U41596; AAC47742.1;
DR	WormPep; F38E1.7; CE04525.
DR	InterPro; IPR000970;
DR	PIfam; PF00110; wnt; 1.
DR	PROSITE; PS00246; WNT1; 1.
KW	Developmental protein; Glycoprotein; signal.
FT	SIGNAL
FT	CHAIN
FT	CARDBYD
FT	CONFLICT
FT	SEQUENCE







DE ACYLHYDROLASE).  
 OS Latiaucanda semifasciata (broad-band-of blue sea snake) (Fishes sea  
 snake).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodactylus; Squamata; Sclerozoa; Serpentes; Colubroidae.  
 OC Latiaucanda; Latiaucandae; Latiaucandini.  
 OX NCBI\_TaxID: 8641.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE: Venom.  
 RX MEDLINE: 8355949; PubMed: 7165732;  
 RA Nishida S., Kim H.S., Tamura N.:  
 RI "Amino acid sequences of three phospholipases A 1, 111 and IV from  
 RI the venom of the sea snake Latiaucanda semifasciata".  
 RL Biochem. J. 267:599-594(1992).  
 CC -1 FUNCTION: PA2 CATALYZES THE CALCIUM DEPENDENT HYDROLYSIS OF THE  
 CC 2 ACYL GROUPS IN 3S PHOSPHOLIPIDS.  
 CC -1 CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O -> 1 ACYLGLYCERYL-  
 CC PHOSPHOCHOLINE + A FATTY ACID ANION.  
 CC -1 SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.  
 DR PIR: A90316; PSUT4E.  
 DR HSSP: P00608; IAE7.  
 DR InterPro: IPR001211; --.  
 DR Pfam: PF00068; phosphlip; 1.  
 DR PRINTS: PR00389; PRPHLPASEA2.  
 DR PROSITE: PS00118; PA2\_HIS; 1.  
 DR PROSITE: PS00119; PA2\_ASP; 1.  
 KW Hydrolyase; Lipid degradation; Calcium; Multigene family; Venom.  
 FT ACT\_SITE 48 48 BY SIMILARITY.  
 FT ACT\_SITE 92 92 BY SIMILARITY.  
 FT DISULFID 11 71 BY SIMILARITY.  
 FT DISULFID 27 117 BY SIMILARITY.  
 FT DISULFID 29 45 BY SIMILARITY.  
 FT DISULFID 44 98 BY SIMILARITY.  
 FT DISULFID 51 91 BY SIMILARITY.  
 FT DISULFID 60 84 BY SIMILARITY.  
 FT DISULFID 78 89 BY SIMILARITY.  
 FT CA\_BIND 49 49 BY SIMILARITY.  
 SQ SEQUENCE 118 AA: 13241 MW: 2749461866CD3B CRC664;

Query Match 61.4% Score 35; DB 1; Length 119;  
 Best Local Similarity 50.0%; Pred. No. 5,2; Mismatches 5; Conservative 3; Caps 0;  
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Caps 0;  
 QY 1 CADDIKCAEC 10  
 DB 89 CACDLEAAEC 98  
 RESULT 7  
 PA2\_OXYSE  
 ID PA2\_OXYSE STANDARD; PRI: 119 AA.  
 AC P00614;  
 DT 21-JUL-1986 (Ref. 01, Created)  
 DT 21-JUL-1986 (Ref. 01, Last sequence update)  
 DT 15-DEC-1998 (Ref. 37, Last annotation update)  
 DE PHOSPHOLIPASE A2, TAIPOXIN ALPHA CHAIN (DP 4.1.1.4)  
 DE (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE).  
 OS Oxynotus scutellatus scutellatus (Australian taipan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodactylus; Squamata; Sclerozoa; Serpentes; Colubroidae.  
 OC Elapidae; Acanthophiinae; Oxynotus.  
 OX NCBI\_TaxID: 8667;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE: Venom.  
 RX MEDLINE: 82261658; PubMed: 7049664;  
 RA Lind P., Fakar D.:  
 RI "Amino acid sequence of the alpha subunit of taipoxin, an extremely  
 RI potent presynaptic neurotoxin from the Australian snake-tailan  
 RI (Oxynotus scutellatus)".  
 RL Eur. J. Biochem. 121:431-437(1982).

CC -1 FUNCTION: TAIPOXIN IS THE MOST POTENT ANIMAL TAIXIN KNOWN.  
 CC THE ALPHA CHAIN HAS POSSESSES A PHOSPHOLIPASE ACTIVITY.  
 CC 1 SUBUNIT, CHAINS THREE NON-COVALENTLY BINDING CHAINS (ALPHA, BETA,  
 CC AND GAMMA), EACH RELATED TO PHOSPHOLIPASE A2.  
 CC -1 MISCELLANEOUS: LD(50) IS 0.4 MG/KG BY INTRAVENOUS INJECTION.  
 CC -1 SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.  
 DR PIR: A30754; I3A.  
 DR HSSP: P00608; IAE7.  
 DR InterPro: IPR001211; --.  
 DR Pfam: PF00068; phosphlip; 1.  
 DR PRINTS: PR00389; PRPHLPASEA2.  
 DR PROSITE: PS00118; PA2\_HIS; 1.  
 DR PROSITE: PS00119; PA2\_ASP; 1.  
 KW Hydrolyase; Lipid degradation; Calcium; Multigene family; Venom.  
 FT ACT\_SITE 48 43 BY SIMILARITY.  
 FT ACT\_SITE 93 94 BY SIMILARITY.  
 FT DISULFID 11 72 BY SIMILARITY.  
 FT DISULFID 27 118 BY SIMILARITY.  
 FT DISULFID 29 45 BY SIMILARITY.  
 FT DISULFID 44 99 BY SIMILARITY.  
 FT DISULFID 51 92 BY SIMILARITY.  
 FT DISULFID 79 85 BY SIMILARITY.  
 FT DISULFID 90 90 BY SIMILARITY.  
 FT CA\_BIND 49 49 BY SIMILARITY.  
 SQ SEQUENCE 119 AA: 13829 MW: 76450061105C03 CRC664;

Query Match 61.4% Score 35; DB 1; Length 119;  
 Best Local Similarity 60.0%; Pred. No. 5,2; Mismatches 6; Conservative 0;  
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Caps 0;  
 QY 1 CADDIKCAEC 10  
 DB 90 CACDLEAAEC 99  
 RESULT 8  
 PPSR\_XENIA  
 ID PPSR\_XENIA STANDARD; PRI: 404 AA.  
 AC Q42586;  
 DT 15-JUL-1998 (Ref. 36, Created)  
 DT 15-JUL-1998 (Ref. 36, Last sequence update)  
 DT 15-DEC-1998 (Ref. 37, Last annotation update)  
 DE 26S PROTEASE REGULATORY SUBUNIT 6A (TAF 6B) PROTEIN 10 (1BP-10).  
 GN TBP10.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID: 8455;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE: Ovary.  
 RX MEDLINE: 98041640; PubMed: 9475782;  
 RA Nacker W.:  
 DE "Members of the AAA gene family are involved in early embryogenesis  
 DE of vertebrates".  
 RL Biochem. Biophys. Acta 1354:1-6(1997).  
 CC -1 FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ACT DEPENDENT  
 CC DEGRADATION OF DEPHOSPHORYLATED TUBULIN. THE REGULATOR OF THE  
 CC COMPLEX COMPLEX AND DEPHOSPHORYLATION ARE SUBSTRATE SPECIFICITY TO THE  
 CC 26S COMPLEX (BY SIMILARITY).  
 CC 1 SUBUNIT MAY FORM A HETERODIMER WITH A RELATED FAMILY MEMBER.  
 CC 1 SUBUNIT MAY FORM A HETERODIMER WITH A RELATED FAMILY MEMBER.  
 CC 1 SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.  
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EMBL: D83522; BAA11949.1; -  
 DR EMBL: D77919; AAB70882.1; ALT\_INIT.  
 DR EMBL: IPR001939; -  
 DR Pfam: PF00004; AAA; 1.  
 DR PROSITE: PS00674; AAA; 1.  
 KW Proteasome; ATP binding; Nuclear protein.  
 FT NPTERM 227 234 AIP (POTENTIAL). 2)  
 FT CONFLICT 84 84 K > N (IN REF. 2).  
 FT CONFLICT 417 417 L > M (IN REF. 2).  
 SQ SEQUENCE 439 AA; 49160 MW; 292E780AE8U19BAE CRC64;

Query Match 61.48; Score 35; DR 1; Length 439;  
 Best Local Similarity 50.08; Pred. No. 18;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAIDKGAFA ID  
 1 1111  
 DB 487 CHIDFNCAGC 496

RESULT 11

ID TIE2\_HUMAN STANDARD; FRT: 1124 AA.  
 AC Q02763;  
 DT 01 FEB 1994 (Ref. 28, Created)  
 DI 01 FEB 1994 (Ref. 29, Last sequence update)  
 DE 01-OCT 2000 (Ref. 40, Last annotation update)  
 DE ANGIOPOIETIN 1 RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE PROTEIN  
 DE KINASE, CELL SURFACE TYPE 2) (TYROSINE KINASE, CELL SURFACE TYPE 2) (EC 2.7.1.112)  
 DE TEK (TIRICA INTERA RECEPTOR, CELL KINASE).  
 GN TEK or TIE2.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI TaxId: 9606.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE placenta;  
 RA Scherfner S.F., Bird L.A., Scherfner J.A., Schooley K.A., Baum P.R.;  
 R1 "Molecular cloning and characterization of a novel receptor protein  
 R1 tyrosine kinase from human placenta."  
 RL Cytosine 8:663-670(1993).  
 RN [2]  
 RP VARIANT VRCM1 TRP 849.  
 RC MEDLINE 97134665; PubMed 8980225;  
 RA Vikkula M., Bock M.M., Cartaway K.L., Hall J., Calvert J.T., Plamondon A.J.,  
 RA Gammie J.B., Pasik W.A., Marth C.A., Watanabe M., Calvert J.T.,  
 RA Mulliken J.B., Olsen P.R.;  
 RA "Vascular dysmorphogenesis caused by an activating mutation in the  
 R1 receptor tyrosine kinase TIE2."  
 RL Cell 87:1181-1190(1996).  
 RN [3]  
 RP VARIANTS VRCM1 TRP-849 AND SER-897.  
 RC MEDLINE 99290443; PubMed 10369874;  
 RA Calvert J.T., Kiley J.J., Kontos G.D., Chu P.H., Prieto V.G.,  
 RA Chen C.R., Bock M.M., Hertz H.G., Simpson S.A., Pasik W.A.,  
 RA Speck M.C., Bock M.M., Hertz H.G., Simpson S.A., Pasik W.A.,  
 RA "Allelic and locus heterogeneity in isolated vascular malformations."  
 RL Hum. Mol. Genet. 8:1279-1289(1999).  
 RN [4]  
 RP RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE RECEPTOR  
 CC MAMMALIAN ENDOTHELIAL CELL LINEAGE MARKER. PROBABLY REGULATES  
 CC ENDOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE  
 CC PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL  
 CC FORMATION.  
 CC CATALYTIC ACTIVITY: AIP + A PROTEIN TYROSINE  
 CC

CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC THESE SEQUENCES ARE SPECIFICALLY EXPRESSED IN ENDOTHELIAL CELLS  
 CC AND THEIR PRECURSORS. THE ANGIOBLASTS HAS BEEN DIRECTLY FOUND  
 CC IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN  
 CC ENDOTHELIAL CELLS, BRAIN AND KIDNEY.  
 CC -1- DISEASE: DEFECTS IN TIE2 ARE A CAUSE OF DOMINANTLY INHERITED  
 CC VENOUS MALFORMATIONS (VMCM1). AN EXCESS OF VASCULAR PROLIFERATION  
 CC CHARACTERIZED BY DILATED, SERPINOUS CHANNELS.  
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC  
 CC DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 PHENOLYL-LIKE C2-TYPE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 DEF-LIKE DOMAINS.  
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 CC EMBL: L06139; AAA61139.1; -  
 DR HSSP: P11362; IPGL.  
 DR MIM: 600221; -  
 DR MIM: 600195; -  
 DR InterPro: IPR000561; -  
 DR InterPro: IPR000719; -  
 DR InterPro: IPR001245; -  
 DR InterPro: IPR001777; -  
 DR Pfam: PF00004; RGF; 2  
 DR Pfam: PF00041; In3; 3.  
 DR Pfam: PF00049; pkinase; 1.  
 DR PR0372; PR0379; TYR KINASE.  
 DR PR0372; PR0379; TYR KINASE.  
 DR PROSITE: PS00109; PROTEIN KINASE TYPE 1.  
 DR PROSITE: PS00611; PROTEIN KINASE TYPE 1.  
 DR PROSITE: PS00022; RGF\_1; 3.  
 DR PROSITE: PS01186; RGF\_2; 3.  
 DR Receptor, Tyrosine Kinase; Transmembrane; Immunoglobulin domain;  
 KW Repeat: EGF-like domain; Transmembrane; Disease mutation.  
 KW Glycoprotein; phosphorylation; Multimeric family; Disease mutation.  
 KW SIGNAL 1 18  
 FT CHAIN 19 1124 ANGIOPOIETIN 1 RECEPTOR.  
 FT E-MAIL 19 745 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 746 770 POTENTIAL.  
 FT SIGNAL 771 1124 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 44 102 IG-LIKE C2-TYPE DOMAIN.  
 FT DOMAIN 210 252 RGF-LIKE 1.  
 FT DOMAIN 254 299 RGF-LIKE 2.  
 FT DOMAIN 301 341 RGF-LIKE 3.  
 FT DOMAIN 370 424 IG-LIKE C2-TYPE DOMAIN.  
 FT DOMAIN 444 536 FIBRONECTIN TYPE III.  
 FT DOMAIN 541 634 FIBRONECTIN TYPE III.  
 FT DOMAIN 638 732 FIBRONECTIN TYPE III.  
 FT DOMAIN 824 1096  
 FT NP\_BIND 830 838  
 FT BINDING 855 855  
 FT ACT\_SITE 964 964  
 FT CATALYTIC 140 340 N-LINKED (GLNAC) (POTENTIAL).  
 FT CATALYTIC 158 158 N-LINKED (GLNAC) (POTENTIAL).  
 FT CATALYTIC 168 168 N-LINKED (GLNAC) (POTENTIAL).  
 FT CATALYTIC 198 198 N-LINKED (GLNAC) (POTENTIAL).  
 FT CATALYTIC 243 243 N-LINKED (GLNAC) (POTENTIAL).  
 FT CATALYTIC 264 264 N-LINKED (GLNAC) (POTENTIAL).  
 FT CATALYTIC 560 560 N-LINKED (GLNAC) (POTENTIAL).  
 FT CATALYTIC 596 596 N-LINKED (GLNAC) (POTENTIAL).  
 FT CATALYTIC 613 613 N-LINKED (GLNAC) (POTENTIAL).  
 FT CATALYTIC 691 691 N-LINKED (GLNAC) (POTENTIAL).  
 FT CATALYTIC 992 992 PHOSPHORYLATION (AUTO-).  
 FT MOD\_RES 992 992 K 33 W (IN VRCM1; ACTIVATING EFFECT).  
 FT VARIANT 849 949 /FTID VAR\_006352.  
 FT VARIANT 997 997 Y 35 (IN VRCM1; ACTIVATING EFFECT).  
 FT



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CC EMBL: L41949; AAA21161.1;
CC BSSP: P01149; IRIG.
CC InterPro: IP0002072; -.
CC EMBL: P000244; NGF_1; -.
CC PROSITE: PS00248; NGF_1; 1.
CC PROSITE: PS00270; NGF_2; 1.
KW Growth factor; Signal.
FT NON_TER 1 1
FT SIGNAL <1 6
FT PROPEP 7 109
FT CHAIN 110 229
FT DISULFID 124 189
FT DISULFID 167 217
FT DISULFID 177 219
FT CARBOHYD 57 57
FT CARBOHYD 102 102
FT CARBOHYD 154 154
SQ SEQUENCE 229 AA; 25275 MW; F8890771CBA3189 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 229;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AIDIKGAE 9
DB 147 AIDIKGAE 144
|||||
ID NGF_BOVIN STANDARD; PRT; 231 AA.
AC P13600; G18969;
DT 01 JAN-1990 (Rel. 13, Created)
DT 15 JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BETA NERVE GROWTH FACTOR PRECURSOR (BETA-NGF) (FRAGMENT).
EN NGF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID 9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: Blood;
RX MEDLINE 97430845; PubMed 9284944;
RA Edouard C., Laurent P., Hayes H., Peddell C., Levezuel H.,
RA Zarazua P.;
RT "Assignment of the beta-nerve growth factor (NGFB) to bovine
RT chromosome 3 band q23 by in situ hybridization.";
RL Cytogenet. Cell Genet. 77:406-407(1997).
RN [2]
RP SEQUENCE OF 107-231 FROM N.A.
RX MEDLINE 86400647; PubMed 2427334;
RA Meier R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;
RT "Molecular cloning of bovine and chick nerve growth factor (NGF);
RT delineation of conserved and unconserved domains and their
RT relationship to the biological activity and antigenicity of NGF.";
RL EMBO J. 5:1489-1493(1986).
CC 1 FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NON-COVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@ebi.ac.uk).
CC
CC EMBL: Y09566; CAA70759.1; -.
CC EMBL: M26809; A26312; A26312.
CC EMBL: A26312; A26312.
CC BSSP: P01139; 1432.
CC InterPro: IPR002072; -.
CC EMBL: P000244; NGF_1; 1.
CC PROSITE: PS00248; NGF_1; 1.
CC PROSITE: PS00270; NGF_2; 1.
KW Growth factor; Signal.
FT NON_TER 1 1
FT SIGNAL <1 8
FT PROPEP 9 111
FT CHAIN 112 231
FT DISULFID 126 191
FT DISULFID 169 219
FT DISULFID 174 221
FT CARBOHYD 154 156
FT CARBOHYD 118 118
FT CONFLICT 161 161
FT CONFLICT 240 231
FT CONFLICT 240 231
SQ SEQUENCE 231 AA; 25437 MW; 01605099291A418C CRC64;

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Query Match 59.6%; Score 34; DB 1; Length 231;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2 AIDIKGAE 9
DB 139 AIDIKGAE 146
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ID NGF_XENLA STANDARD; PRT; 231 AA.
AC P21617;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE NERVE GROWTH FACTOR PRECURSOR (NGF).
EN Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8455;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 91362944; PubMed=1888511;
RA Carriero P., Campioni M., Cardinali B., Pierandrei-Analdi P.;
RT "Structure and expression of the nerve growth factor gene in Xenopus
RT oocytes and embryos.";
RL Mol. Reprod. Dev. 29:313-322(1991).
RN [2]
RP SEQUENCE OF 170-211 FROM N.A.
RC TISSUE: Liver;
RX MEDLINE 91225573; PubMed 2025430;
RA Hallböök F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary.";
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NON-COVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC
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CC -----  
 DR EMBL: X55710; CAA49249.1; ALT\_INIT.  
 DR PIR: S14481; S14481.  
 DR RSPV: FullCo: USGF.  
 DR InterPro: IPR002072; -.  
 DR PTam: PF00243; NGE\_1.  
 DR PRINTS: PR01268; NGE.  
 DR PROSITE: PS0248; NGE\_1; 1.  
 DR PROSITE: PS0270; NGE\_2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT PROPEP 19 114 POTENTIAL.  
 FT CHAIN 115 231 NERVE GROWTH FACTOR.  
 FT DISULFID 128 194 BY SIMILARITY.  
 FT DISULFID 171 221 BY SIMILARITY.  
 FT DISULFID 181 223 BY SIMILARITY.  
 FT CARBOHYD 64 63 N LINKED (GLYNA1...) (POTENTIAL).  
 FT CARBOHYD 107 107 N LINKED (GLYNA1...) (POTENTIAL).  
 FT CARBOHYD 158 158 N LINKED (GLYNA1...) (POTENTIAL).  
 SQ SEQUENCE 231 AA; 26416 MW; 72A04E7D00B8605 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 231  
 Best Local Similarity 87.9%; Prod. No. 15;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 ATRKCAF 9  
 IB 141 ATRKCF 148

Search completed: August 30, 2001, 16:32:00  
 Job time: 58 sec

A:Residues: 1-118 <NIS>

C:Function:

A:Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycerol-phosphocholine to 1-acyl-sn-glycerol; the reaction is strongly enhanced when the phospholipid is condensed into a micelle

C:Superfamily: phospholipase A2

C:Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; protein

F:4,67/Binding site: carboxyl substrate (Gln, Tyr) #status predicted

F:11,27,117,29,45,44,98,51,91,60,94,79-89/Binding site: calcium (Tyr, Gly, Asp) #status predicted

F:28,40,42,49/Binding site: calcium (Tyr, Gly, Asp) #status predicted

F:48,92/Active site: His, Asp #status predicted

Query Match 61.4% Score 35; DB 1; Length 118;

Best Local Similarity 50.0% Pred. No. 16;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEK 10

II III I I I

DB 89 CACDLEAAKC 98

RESULT 7

PSI14E

phospholipase A2 (EC 3.1.1.4) IV - broad-banded blue sea krait

N:Alternative names: phosphatidylcholine 2-acylhydrolase

C:Species: Latiauda semifasciata (broad-banded blue sea krait, etabu sea snake)

C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 28-Feb-1997

C:Accession: A90316; A00753

R:Nishida, S.; Kim, H.S.; Tamiya, N.

Biochem. J. 207, 589-594, 1982

A:Title: Amino acid sequences of three phospholipases A 1, III and IV from the venom of

A:Reference number: A90316; MUID:84153048

A:Accession: A90316

A:Molecule type: protein

A:Residues: 1-118 <NIS>

C:Function:

A:Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycerol-phosphocholine to 1-acyl-sn-glycerol; the reaction is strongly enhanced when the phospholipid is condensed into a micelle

C:Superfamily: phospholipase A2

C:Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; protein

F:4,67/Binding site: carboxyl substrate (Gln, Tyr) #status predicted

F:11,27,117,29,45,44,98,51,91,60,94,79-89/Binding site: calcium (Tyr, Gly, Asp) #status predicted

F:28,40,42,49/Binding site: calcium (Tyr, Gly, Asp) #status predicted

F:48,92/Active site: His, Asp #status predicted

Query Match 61.4% Score 35; DB 1; Length 118;

Best Local Similarity 50.0% Pred. No. 16;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEK 10

II III I I I

DB 89 CACDLEAAKC 98

RESULT 8

PSI11E

phospholipase A2 (EC 3.1.1.4) I - broad banded blue sea krait

N:Alternative names: phosphatidylcholine 2-acylhydrolase

C:Species: Latiauda semifasciata (broad-banded blue sea krait, etabu sea snake)

C:Date: 02-Apr-1982 #sequence\_revision 31-Dec-1989 #text\_change 28-Feb-1997

C:Accession: A94325; A00752; A08021

R:Ikusaka, G.; Kurauchi, H.; Shikama, T.; Tamiya, N.

Toxicon 26, 747-749, 1988

A:Title: Correction of amino acid sequence of phospholipase A 2 I from the venom of Latiauda

A:Reference number: A94325; MUID:89044898

A:Accession: A94325

A:Molecule type: protein

A:Residues: 1-118 <IAK>

R:Nishida, S.; Kim, H.S.; Tamiya, N.

Biochem. J. 207, 589-594, 1982

A:Title: Amino acid sequences of three phospholipases A 1, III and IV from the venom of

A:Reference number: A90316; MUID:84153048

A:Contents: annotation; specific activity

A:Note: Trp 64 is important to enzyme activity

C:Function:

A:Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycerol-phosphocholine to 1-acyl-sn-glycerol; the reaction is strongly enhanced when the phospholipid is condensed into a micelle

C:Superfamily: phospholipase A2

C:Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; protein

F:4,67/Binding site: carboxyl substrate (Gln, Tyr) #status predicted

F:11,27,117,29,45,44,98,51,91,60,94,79-89/Binding site: calcium (Tyr, Gly, Asp) #status predicted

F:28,40,42,49/Binding site: calcium (Tyr, Gly, Asp) #status predicted

F:48,92/Active site: His, Asp #status predicted

Query Match 61.4% Score 35; DB 1; Length 118;

Best Local Similarity 50.0% Pred. No. 16;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEK 10

II III I I I

DB 89 CACDLEAAKC 98

RESULT 9

PSOXA

phospholipase A2 (EC 3.1.1.4) taipoxin alpha chain Australian taipan

N:Alternative names: phosphatidylcholine 2-acylhydrolase

C:Species: Oxyuranus scutellatus scutellatus (Australian taipan)

C:Date: 14-Nov-1993 #sequence\_revision 11-Nov-1993 #text\_change 28-Feb-1997

C:Accession: A00754

R:Bind, P.; Baker, D.

Eur. J. Biochem. 124, 441-447, 1982

A:Title: Amino acid sequence of the alpha-subunit of taipoxin, an extremely potent pr

A:Reference number: A00754; MUID:82261658

A:Accession: A00754

A:Molecule type: protein

A:Residues: 1-119 <LIN>

C:Function:

A:Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycerol-phosphocholine to 1-acyl-sn-glycerol; the reaction is strongly enhanced when the phospholipid is condensed into a micelle

C:Superfamily: phospholipase A2

C:Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; protein

F:4,67/Binding site: carboxyl substrate (Gln, Tyr) #status predicted

F:11,27,117,29,45,44,98,51,91,60,94,79-89/Binding site: calcium (Tyr, Gly, Asp) #status predicted

F:28,40,42,49/Binding site: calcium (Tyr, Gly, Asp) #status predicted

F:48,92/Active site: His, Asp #status predicted

Query Match 61.4% Score 35; DB 1; Length 118;

Best Local Similarity 50.0% Pred. No. 16;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEK 10

II III I I I

DB 90 CACDLEAAKC 99

RESULT 10

PSI11E

fat-binding protein-1 - human

C:Species: Homo Sapiens (man)

C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 19-Jun-2001

C:Accession: A34842

R:Belikov, P.; Filippov, P.; Perkins, A.; Rosen, C.A.

Science 248, 1650-1653, 1990

A:Title: A cDNA for a protein that interacts with the human immunodeficiency virus tat

A:Reference number: A34842; MUID:90302011

A:Accession: A34842

A:Molecule type: mRNA

A:Residues: 1-404 <NELS>

C:Accession: A34842

C:Species: Homo Sapiens (man)

C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 19-Jun-2001

C:Accession: A34842

A:Title: A cDNA for a protein that interacts with the human immunodeficiency virus tat

A:Reference number: A34842; MUID:90302011

A:Accession: A34842

A:Molecule type: mRNA

A:Residues: 1-404 <NELS>

C:Accession: A34842

C:Species: Homo Sapiens (man)

F1165 47% homology: F1165/US09-018-194-9.rpr type: ATP-binding domain homology - VADP  
 F1192 100% homology: nucleotide binding motif A (P-loop)

Query Match 61.4% Score 35; 108 2; Length 404;  
 Best Local Similarity 60.0%; Prod. No. 48;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATHIKAE 10  
 1 1 1 1 1  
 IR 46 CATHIKAE 46

## RESULT 11

133155

hypothetical protein F56H1.4 Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29 Oct 1999 #sequence revision 29-Oct-1999 #text change 31 Jan-2000

C:Accession: 133155

RefSeq: F1

submitted to the EMBL Data Library, May 1999

A:Description: The sequence of C. elegans (cosmid F56H1).

A:Reference number: Z21294

A:Accession: 133155

A>Status: preliminary; translated from cDNA/F56H1.4

A:Molecule type: DNA

A:Residues: 1340 (GAA)

A:Cross references: EMBL:AF067618; F1192/AA019196.1; GSPR:G000000000; CESP:F56H1.4

A:Experimental source: strain Bristol N2; clone F56H1

C:Genetics:

A:Map position: 1

A:Insertions: 2217; 4973; 6772

C:Superfamily: ATP dependent 26S proteinase; F1192/2912/AA019196.1 type: ATP-binding domain

## Query Match

61.4% Score 35; 108 2; Length 129;

Best Local Similarity 60.0%; Prod. No. 51;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATHIKAE 10  
 1 1 1 1 1  
 IR 478 CATHIKAE 487

## RESULT 12

118974

hypothetical protein C06A1.4 Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15 Oct 1999 #sequence revision 15-Oct-1999 #text change 31 Jan-2000

C:Accession: 118974

RefSeq: F1

submitted to the EMBL Data Library, June 1995

A:Reference number: Z19054

A:Accession: 118974

A>Status: preliminary; translated from cDNA/C06A1.4

A:Molecule type: DNA

A:Residues: 1340 (GAA)

A:Cross references: EMBL:Z43486; F1192/AA05054.1; GSPR:G000000000; CESP:C06A1.4

A:Experimental source: clone C06A1

C:Genetics:

A:Map position: 1

A:Insertions: 2217; 4973; 6772

C:Superfamily: ATP dependent 26S proteinase; F1192/2912/AA019196.1 type: ATP-binding domain

## Query Match

61.4% Score 35; 108 2; Length 49;

Best Local Similarity 60.0%; Prod. No. 48;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATHIKAE 10  
 1 1 1 1 1  
 IR 417 CATHIKAE 426

## RESULT 13

122944

hypothetical protein F56H1.4 Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15 Oct 1999 #sequence revision 15-Oct-1999 #text change 31 Jan-2000

C:Accession: 122944

RefSeq: F1

submitted to the EMBL Data Library, November 1999

A:Reference number: Z19054

A:Accession: 122944

A>Status: preliminary; translated from cDNA/F56H1.4

A:Molecule type: DNA

A:Residues: 1340 (GAA)

A:Cross references: EMBL:AF067618; F1192/AA019196.1; GSPR:G000000000; CESP:F56H1.4

A:Experimental source: strain Bristol N2; clone F56H1

C:Genetics:

A:Map position: 1

A:Insertions: 2217; 4973; 6772

C:Superfamily: ATP dependent 26S proteinase; F1192/2912/AA019196.1 type: ATP-binding domain

## Query Match

61.4% Score 35; 108 2; Length 404;

Best Local Similarity 60.0%; Prod. No. 48;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATHIKAE 10  
 1 1 1 1 1  
 IR 417 CATHIKAE 426

## RESULT 14

134172

Ca2+ Transporting ATPase (P4-ATPase)

C:Species: Mytilus edulis

C:Date: 22 Apr 1999 #sequence revision 22-Apr-1999 #text change 31 May 2000

C:Accession: 134172

RefSeq: X1

submitted to the EMBL Data Library, May 1999

A:Reference number: Z19054

A:Accession: 134172

A>Status: translated from cDNA/134172

A:Molecule type: DNA

A:Residues: 1340 (GAA)

A:Cross references: EMBL:Z43486; F1192/AA05054.1; GSPR:G000000000; CESP:134172

A:Experimental source: cDNA/134172

C:Genetics:

A:Map position: 1

A:Insertions: 2217; 4973; 6772

C:Superfamily: Na+/K+ Transporting ATPase alpha chain; Amino acid sequence: P4-ATPase

C:Keywords: hydrolase; calcium binding; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

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F1192/2912/AA019196.1; status predicted: 7A1;

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F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

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F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

F1192/2912/AA019196.1; status predicted: 7A1;

protein-tyrosine kinase (EC 2.7.1.122), receptor type tek precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #ext\_change 16-Jul-1999  
 C:Accession: 158488  
 R:Ziegler, S.F.; Bird, J.A.; Scherlinger, J.A.; Schooley, K.A.; Baum, P.R.  
 Oncogene 6, 663-670, 1993  
 A:Title: Molecular cloning and characterization of a novel receptor protein tyrosine kin  
 A:Reference number: 158488; M01D:94173509  
 A:Accession: 158488  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1124 <RES>  
 A:Cross-references: GB:L06139; NID:q292923; P1DN:AAA61199.1; PID:q292924  
 C:Genetics:  
 A:Gene: GDR:TEK  
 A:Cross-references: GDR:344185; OMIM:600221  
 A:Map position: 9p21-9p21  
 C:Function:  
 A:Description: catalyzes the phosphorylation of a peptide! tyrosine residue by ATP  
 C:Similarity: protein tyrosine kinase, receptor type tek, EGF homology, fibroblast tyb  
 C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-1124/Repeat: protein tyrosine kinase, receptor type tek #status predicted <WAT>  
 F:47-104/Domain: immunoglobulin homology <IM1>  
 F:145-147/Repeat: cell attachment (R-G-b) motif  
 F:211-261/Domain: EGF homology <EG1>  
 F:265-298/Domain: EGF homology <EG2>  
 F:302-340/Domain: EGF homology <EG3>  
 F:344-426/Domain: immunoglobulin homology <IM2>  
 F:447-527/Domain: fibroblast type III repeat homology <FNSA>  
 F:542-625/Domain: fibroblast type III repeat homology <FNSB>  
 F:630-720/Domain: fibroblast type III repeat homology <FNAC>  
 F:752-772/Domain: transmembrane #status predicted <TM6>  
 F:822-1094/Domain: protein kinase homology <KIN>  
 F:840-858/Repeat: protein kinase ATP-binding motif  
 F:140-158, 399, 448, 464, 560, 596, 649, 691/Binding site: carbohydrate (Asn) (covalent) #statu  
 F:855, 872, 964/Active site: Lys, Glu, Asp #status predicted

Query Match 61.4%; Score 35; DB 1; Length 1124;

Best local similarity 60.0%; Pred. No. 1.2e+02;

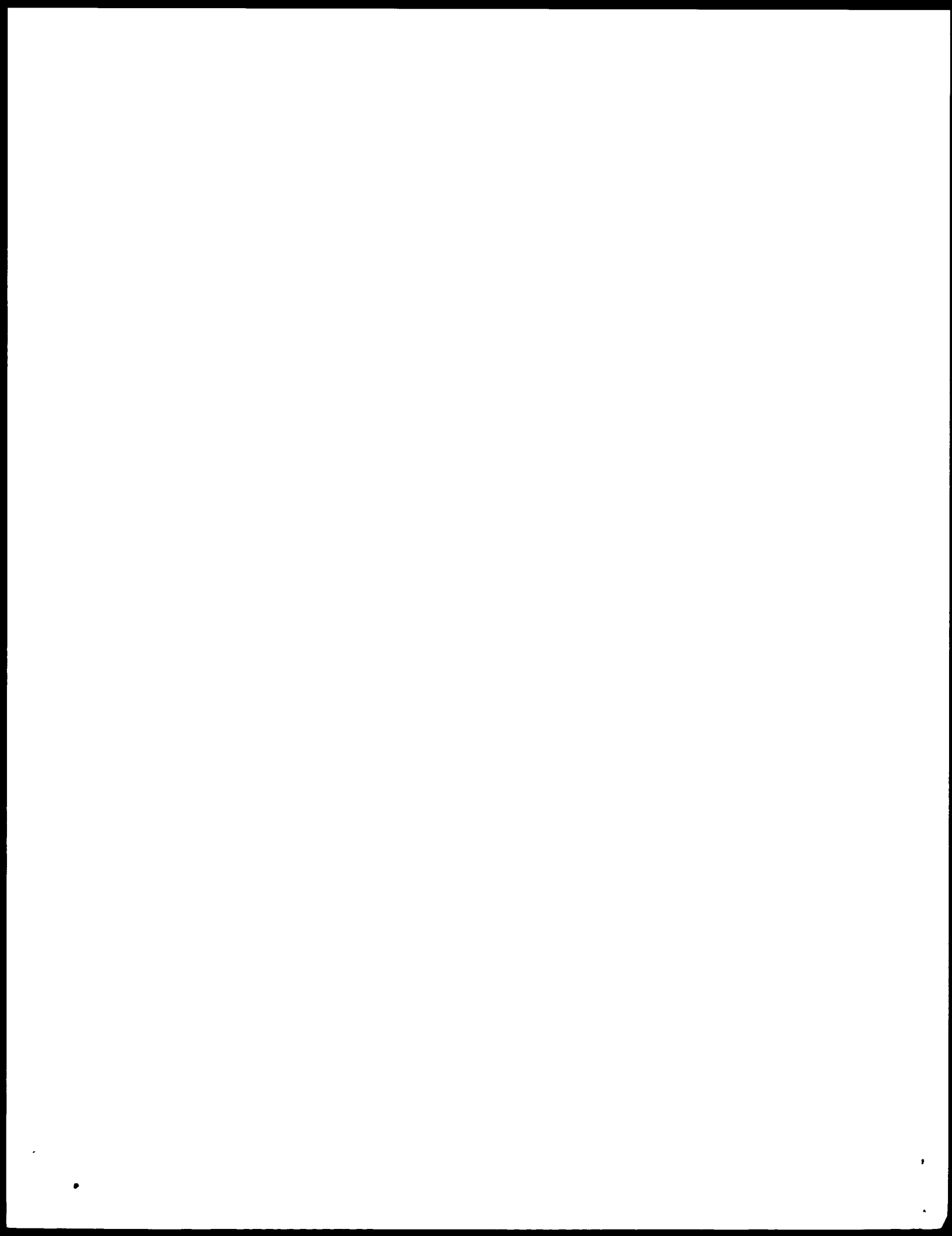
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDVKGAGC 10

Db 289 CATGWKGLQC 298

Search completed: August 30, 2001, 16:31:44

Job time: 4.2 sec





QY 1 'AALDKGAB' 10  
111 11 11  
DB 447 CAGYKQWJQ 446

## RESULT 2

US-08-696-854B-5  
Sequence 2, Application US/0842474  
Patent No. 5437660  
GENERAL INFORMATION:  
APPLICANT: Ziegler, Steven F.  
TITLE OF INVENTION: NOVEL TYROSINE KINASE  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 61 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version # 1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 05/0842474  
FILING DATE: 05/08/2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/905,600  
FILING DATE: 26 JUN 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seesoo, Kathryn A.  
REGISTRATION NUMBER: 42,172  
REFERENCE/ACKNOWLEDGMENT NUMBER: 2609  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 243-0644  
TELEX: 766822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1124 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-696-854B-5

Query Match 61.4% Score 45: DB 1: Length 1124;  
Best Local Similarity 60.0% Pred. No. 1.4e+02;  
Matches 6: conservative 1: Mismatches 4: Indels 0: Gaps 0;

QY 1 'AALDKGAB' 10  
111 11 11  
DB 289 CAGYKQWJQ 298

## RESULT 3

US-08-696-854B-5  
Sequence 2, Application US/0842474  
Patent No. 5437660  
GENERAL INFORMATION:  
APPLICANT: Ziegler, Steven F.  
TITLE OF INVENTION: NOVEL TYROSINE KINASE  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 61 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version # 1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 05/0842474  
FILING DATE: 05/08/2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/905,600  
FILING DATE: 26 JUN 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seesoo, Kathryn A.  
REGISTRATION NUMBER: 42,172  
REFERENCE/ACKNOWLEDGMENT NUMBER: 2609  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 243-0644  
TELEX: 766822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1124 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-696-854B-5

Query Match 61.4% Score 45: DB 1: Length 1124;  
Best Local Similarity 60.0% Pred. No. 1.4e+02;  
Matches 6: conservative 1: Mismatches 4: Indels 0: Gaps 0;

QY 1 'AALDKGAB' 10  
111 11 11  
DB 289 CAGYKQWJQ 298

## RESULT 4

US-08-696-854B-5  
Sequence 2, Application US/0842474  
Patent No. 5437660  
GENERAL INFORMATION:  
APPLICANT: SARADAT, D. H.  
APPLICANT: Desai, Lynne  
APPLICANT: Chellappa, Claudio A.  
TITLE OF INVENTION: SERVE GROWTH FACTOR RECEPTOR ANALOGS  
TITLE OF INVENTION: AND THEIR USES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: KLAUFER & JACKSON  
STREET: Commercial Plaza, 411 Hackensack Avenue  
CITY: Hackensack  
STATE: N.J.  
COUNTRY: U.S.A.  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version # 1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 05/0842474  
FILING DATE: 07 JUL 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 05/0842474  
FILING DATE: 07 JUL 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: JACKSON, David A.  
REGISTRATION NUMBER: 26,742  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (201) 487-5800  
 TELEFAX: (201) 343-1684  
 TELEX: 143521  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-696-854B-5

Query Match 59.6%; Score 34; DB 3; Length 9;  
 Best Local Similarity 87.5%; Pred. No. 1,540,059;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AIDKGAE 9  
 DB 1 AIDKKEE 8

RESULT 5  
 US-08-696-854B-2  
 Sequence 2, Application US/08696854B  
 Patent No. 6017878  
 GENERAL INFORMATION:  
 APPLICANT: SARAGOV, Uri H.  
 APPLICANT: LESAGEUR, Lynne  
 APPLICANT: CURIELLO, Claudio A.  
 TITLE OF INVENTION: NERVE GROWTH FACTOR STRUCTURAL ANALYSIS  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KLAIPER & JACKSON  
 STREET: Continental Plaza, 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: N.J.  
 COUNTRY: U.S.A.  
 ZIP: 07601  
 COMPUTER RELEASABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/696,854B  
 FILING DATE: 07-AUG-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/CA95/00059  
 FILING DATE: 07-FEB-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9402331.4  
 FILING DATE: 07-FEB-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JACKSON, David A.  
 REGISTRATION NUMBER: 26,742  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (201) 487-5800  
 TELEFAX: (201) 343-1684  
 TELEX: 143521  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Modified site  
 LOCATION: one of (1,10)  
 OTHER INFORMATION: \*Xaa is any uncharged amino acid  
 OTHER INFORMATION: or hydrophobic amine acid"

US-08-696-854B-2

Query Match 59.6%; Score 34; DB 4; Length 13;  
 Best Local Similarity 85.7%; Pred. No. 1,947,369;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AIDKGAEE 9  
 DB 3 AIDKKEC 9

RESULT 6  
 US-07-847-369-1  
 Sequence 1, Application US/07847369  
 Patent No. 5449055  
 GENERAL INFORMATION:  
 APPLICANT: PERSSON, Hakan B. et al.  
 TITLE OF INVENTION: Neurotrophic Factors Having Altered Receptor Binding Specificities  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Eichenon Pharmaceuticals, Inc.  
 STREET: 7771 14 Saw Mill River Road  
 CITY: Larchmont  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10591-6707  
 COMPUTER RELEASABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/847,369  
 FILING DATE: 19920306  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Koppell, Gail M./Mistock, S. Leslie  
 REGISTRATION NUMBER: 32,113/18,872  
 REFERENCE CITE NUMBER: 6526-097  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 914-347-7000  
 FAX: 914-347-2113  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: AMINO ACID  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-07-847-369-1

Query Match 59.6%; Score 34; DB 1; Length 12;  
 Best Local Similarity 87.5%; Pred. No. 2,231,369;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AIDKGAEE 9  
 DB 4 AIDKKEE 11

RESULT 7  
 US-07-847-369-2  
 Sequence 2, Application US/07847369  
 Patent No. 5449055  
 GENERAL INFORMATION:  
 APPLICANT: PERSSON, Hakan B. et al.  
 TITLE OF INVENTION: Neurotrophic Factors Having Altered Receptor Binding Specificities  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
 STREET: 777 Old Saw Mill River Road  
 CITY: Tarrytown  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10591-6707  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 05/07/847,369  
 FILING DATE: 19920406  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Komplet, Gail M./Mistock, S. Leslie  
 REGISTRATION NUMBER: 32,143/18,972  
 REFERENCE/BOOK NUMBER: 6526-097  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 914 347-7000  
 TELEFAX: 914 347-2113  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: AMINO ACID  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-07 847 369 2

Query Match 59.68; Score 34; DB 1; Length 12;  
 Best Local Similarity 87.5%; Pred. No. 2.2;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGAE 9  
 DB 4 ATDIKGKE 11  
 RESULT 8  
 US-08-400-044-1  
 Sequence 1, Application US/08400044  
 Patent No. 5705617  
 GENERAL INFORMATION:  
 APPLICANT: Persson, Hakan B. et al.  
 TITLE OF INVENTION: Neurotrophic Factors Having Altered  
 TITLE OF INVENTION: Receptor Binding Specificities  
 NUMBER OF SEQUENCES: 6  
 CURRENT SEQUENCE ADDRESS:  
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
 STREET: 777 Old Saw Mill River Road  
 CITY: Tarrytown  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10591-6707  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 05/08/400,044  
 FILING DATE: 02-SEP-1994  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/847,369  
 FILING DATE: 06-MAR-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Komplet, Gail M./Mistock, S. Leslie  
 REGISTRATION NUMBER: 32,143/18,972  
 REFERENCE/BOOK NUMBER: 6526-097

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 914 347-7000  
 TELEFAX: 914 347-2113  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-400-044-1

Query Match 59.68; Score 34; DB 1; Length 12;  
 Best Local Similarity 87.5%; Pred. No. 2.2;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGAE 9  
 DB 4 ATDIKGKE 11  
 RESULT 9  
 US-08-400-044-2

Sequence 2, Application US/08400044  
 Patent No. 5705617  
 GENERAL INFORMATION:  
 APPLICANT: Persson, Hakan B. et al.  
 TITLE OF INVENTION: Neurotrophic Factors Having Altered  
 TITLE OF INVENTION: Receptor Binding Specificities  
 NUMBER OF SEQUENCES: 6  
 CURRENT SEQUENCE ADDRESS:  
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
 STREET: 777 Old Saw Mill River Road  
 CITY: Tarrytown  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10591-6707  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 05/08/400,044  
 FILING DATE: 02-SEP-1994  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/847,369  
 FILING DATE: 06-MAR-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Komplet, Gail M./Mistock, S. Leslie  
 REGISTRATION NUMBER: 32,143/18,972  
 REFERENCE/BOOK NUMBER: 6526-097  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 914 347-7000  
 TELEFAX: 914 347-2113  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-400-044-2

Query Match 59.68; Score 34; DB 1; Length 12;  
 Best Local Similarity 87.5%; Pred. No. 2.2;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGAE 9  
 DB 4 ATDIKGKE 11

```

DB      4  AADIKGKE 11
RESULT 10
US-08-753-642-2
Sequence 2, Application US/08753642
Patent No. 6003757
GENERAL INFORMATION:
APPLICANT: HRSO, RICHARD G.
TITLE OF INVENTION: WOUND TREATMENT METHOD WITH NERVE GROWTH
FACTORS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94040-1018
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,642
FILING DATE: 27-NOV-1996
CLASSIFICATION: 51A
ATTORNEY/AGENT INFORMATION:
NAME: MUNROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 32718-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSNIOERS SFO
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US 08 753 642-2

Query Match: 59.6%; Score 34; DB 3; Length 119;
Best Local Similarity: 87.5%; Pred. No. 23;
Matches: 7; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

QY      2  AADIKGAE 9
DB      29  AADIKGKE 46
RESULT 11
US-07-979-630-1
Sequence 1, Application US/07979630
Patent No. 5488099
GENERAL INFORMATION:
APPLICANT: Persson, et al.
TITLE OF INVENTION: Multifunctional Neurotrophic Factors
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match: 59.6%; Score 34; DB 3; Length 119;
Best Local Similarity: 87.5%; Pred. No. 23;
Matches: 7; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

QY      2  AADIKGAE 9
DB      29  AADIKGKE 46
RESULT 12
US-08-440-049-1
Sequence 1, Application us/08440049
Patent No. 5728804
GENERAL INFORMATION:
APPLICANT: Dried, Roman
APPLICANT: Prestia, Leonard G.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: PANCREATIC NEUROTROPHIC FACTORS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPat In (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/98/440,049
FILING DATE: 12-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253947
FILING DATE: 05-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P090502
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-8674
TELEFAX: 415/252-9881
TELEX: 910931 7168
INFORMATION FOR SEQ ID NO: 1:

```

SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TORDLOGY: Linear  
US-08 440 049 1

Query Match 59.68; Score 34; DB 1; Length 120;  
Best Local Similarity 87.58; Prod. No. 24;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AIDIKGAE 9  
DB 28 AIDIKGE 45

RESULT 14  
US-08 440 049-3  
Sequence 3, Application US/08440049

PATENT NO. 5981480  
GENERAL INFORMATION:  
APPLICANT: Interz, Roman  
APPLICANT: Presta, Leonard G.  
APPLICANT: Winslow, John W.  
TITLE OF INVENTION: PANCREATIC NEUROTROPHIC FACTORS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENT ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,049  
FILING DATE: 12 May 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/25,947  
FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 46,700  
REFERENCE/PICKET NUMBER: P090502  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/225-8674  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TORDLOGY: Linear  
US-08 440 049 3

Query Match 59.68; Score 34; DB 1; Length 120;  
Best Local Similarity 87.58; Prod. No. 24;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AIDIKGAE 9  
DB 28 AIDIKGE 45

RESULT 14  
US-08 441 513A 1  
Sequence 1, Application US/08441513A

PATENT NO. 5981480  
GENERAL INFORMATION:  
APPLICANT: Interz, Roman  
APPLICANT: Presta, Leonard G.  
APPLICANT: Winslow, John W.  
TITLE OF INVENTION: PANCREATIC NEUROTROPHIC FACTORS  
NUMBER OF SEQUENCES: 20  
CORRESPONDENT ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,513A  
FILING DATE: 15 May 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/25,947  
FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 46,700  
REFERENCE/PICKET NUMBER: P090504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/225-8674  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TORDLOGY: Linear  
US-08 441 513A 1

Query Match 59.68; Score 34; DB 2; Length 120;  
Best Local Similarity 87.58; Prod. No. 24;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AIDIKGAE 9  
DB 28 AIDIKGE 45

RESULT 15  
US-08 441 513A 3  
Sequence 3, Application US/08441513A

PATENT NO. 5981480  
GENERAL INFORMATION:  
APPLICANT: Interz, Roman  
APPLICANT: Presta, Leonard G.  
APPLICANT: Winslow, John W.  
TITLE OF INVENTION: PANCREATIC NEUROTROPHIC FACTORS  
NUMBER OF SEQUENCES: 20  
CORRESPONDENT ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/25,947  
FILING DATE: 15 May 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/25,947  
FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Timothy E.  
REGISTRATION NUMBER: 46,700  
REFERENCE/PICKET NUMBER: P090502  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8674  
TELEFAX: 415/225-8674  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TORDLOGY: Linear  
US-08 441 513A 3

Thu Aug 30 16:34:17 2001

APPLICATION NUMBER: 09/09/441.513A  
FILING DATE: 15-May-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/253937  
FILING DATE: 03-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 46,790  
REFERENCE/BOOKET NUMBER: P0905C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
Topology: Linear  
US: 08-441-513A 3

Query Match 59.6%; Score 34; DB 2; Length 120;  
Best Local Similarity 87.5%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 ADDIKGAE 9  
106 28 ADDIKGKE 35

Search completed. August 30, 2001, 16:32:47  
Job time: 105 sec













DR InterPro: IP001211; -.  
 DR Pfam: PF00068; phospho 1.  
 DR PRINTS: PR00489; PPHILIPASEA2.  
 DR PRODOM: P000404; -. 1.  
 DR PROSITE: PS00119; PA2\_ASP; 1.  
 DR PROSITE: PS00118; PA2\_HIS; 1.  
 DR SMART: SM00085; PA2c; 1.  
 KW Signal.  
 FT SIGNAL 1 27  
 ST SEQUENCE 145 AA: 16073 MW: 49048439160F7805 CRC64;

Query Match 61.4%; Score 35; DB 13; Length 145;  
 Best Local Similarity 50.0%; Pred. No. 19;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEE 10  
 ||| ||| |||  
 DB 116 CADIQAAKE 125

RESULT 14

Q01843 PRELIMINARY: PRT: 145 AA.  
 A\* Q01843;

DT 01 OCT-2000 (TFMBLrel. 15, Created)

DT 01 OCT-2000 (TFMBLrel. 15, Last sequence update)

DT 01 MAR-2001 (TFMBLrel. 16, Last annotation update)

DE PHOSPHOLIPASE A2 PRECURSOR.

GN PLA2.

OS Latuca somitasciata (Broad-banded blue sea snake) (Draba sea

snake).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Serpentes; Colubridae;

OC Elapidae; Latucaudinae; Latucauda.

OX NCBI\_TaxID=8641;

KN [1]

RN SEQUENCE FROM N.A.

RC TISSUE=VENOM GLAND;

RA Tamiya T., Fujimi T.J.J.

RT "Latuca somitasciata phospholipase A2 cDNA clone ISP-A2c1p05,"

SL Submitted (JAN 2000) to the EMBL/GenBank/CCRC databases.

DR EMBL: AR037413; BAB03300.1; -.  
 DR InterPro: IP001211; -.  
 DR Pfam: PF00068; phospho 1.  
 DR PRINTS: PR00489; PPHILIPASEA2.  
 DR PRODOM: P000404; -. 1.  
 DR PROSITE: PS00119; PA2\_ASP; 1.  
 DR PROSITE: PS00118; PA2\_HIS; 1.  
 DR SMART: SM00085; PA2c; 1.  
 KW Signal.  
 FT SIGNAL 1 27  
 ST SEQUENCE 145 AA: 16073 MW: 9260E8861DE887 CRC64;

Query Match 61.4%; Score 35; DB 13; Length 145;  
 Best Local Similarity 50.0%; Pred. No. 19;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEE 10  
 ||| ||| |||  
 DB 116 CADIQAAKE 125

RESULT 15

Q01842 PRELIMINARY: PRT: 145 AA.  
 A\* Q01842;

DT 01 OCT-2000 (TFMBLrel. 15, Created)

DT 01 OCT-2000 (TFMBLrel. 15, Last sequence update)

DT 01 MAR-2001 (TFMBLrel. 16, Last annotation update)

DE PHOSPHOLIPASE A2 PRECURSOR.

GN PLA2.

OS Latuca somitasciata (Broad-banded blue sea snake) (Draba sea  
 snake).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Serpentes; Colubridae;  
 OC Elapidae; Latucaudinae; Latucauda.  
 OX NCBI\_TaxID=8641;  
 KN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=VENOM GLAND;  
 RA Tamiya T., Fujimi T.J.J.  
 RT "Latuca somitasciata phospholipase A2 cDNA clone ISP-A2c1p05,"  
 SL Submitted (JAN 2000) to the EMBL/GenBank/CCRC databases.

DR EMBL: AR037413; BAB03300.1; -.  
 DR InterPro: IP001211; -.  
 DR Pfam: PF00068; phospho 1.  
 DR PRINTS: PR00489; PPHILIPASEA2.  
 DR PRODOM: P000404; -. 1.  
 DR PROSITE: PS00119; PA2\_ASP; 1.  
 DR PROSITE: PS00118; PA2\_HIS; 1.  
 DR SMART: SM00085; PA2c; 1.  
 KW Signal.  
 FT SIGNAL 1 27  
 ST SEQUENCE 145 AA: 16073 MW: 9260E8861DE887 CRC64;

Query Match 61.4%; Score 35; DB 13; Length 145;  
 Best Local Similarity 50.0%; Pred. No. 19;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEE 10  
 ||| ||| |||  
 DB 116 CADIQAAKE 125

Search completed: August 30, 2001, 16:42:29  
 Job time: 87 sec

us-09-018-194-9.rspt

Thu Aug 30 16:34:20 2001







FI Protein 473..704  
 FI /note: "pe portion"  
 PN W0250075423-A1.  
 XX 14 DEC-2000.  
 XX 07-JUN-2000; 2000W0-US15706.  
 AA 07-JUN-1999; 990S-0147889.  
 XX (IMMUNEX CORP.  
 XX Corretti DP, Borges LG, Fanslow WC;  
 XX WPI; 2001 112149/12.  
 XX New tek polypeptide is a polypeptide having a fragment of the tek  
 PI extracellular domain, useful for treating mammals with a disease  
 PI mediated by angiogenesis, e.g. tumors, ocular neovascularization or  
 PI inflammatory diseases.  
 XX Claim 17, Page 47-49; 43pp; English.  
 PS The present sequence represents a fusion protein comprising the  
 CC extracellular domain of the human receptor tyrosine kinase and the  
 CC portion of human immunoglobulin (Ig) G1. The tek fragment lacks all  
 CC or part of the region containing fibronectin type III (FNIII) motifs, and  
 CC retains the ability to bind at least one tek ligand. The fusion  
 CC polypeptide is an angiogenesis inhibitor, and a tek antagonist.  
 CC retinopathy is an angiogenesis inhibitor, antibodies or antibody fragments are  
 CC useful for treating a mammal having a disease or condition mediated by  
 CC angiogenesis, e.g. a solid tumor, a condition of disease characterized by  
 CC ocular neovascularization. In particular, the tek antagonists are useful  
 CC for treating or preventing inflammatory diseases (e.g. arthritis,  
 CC rheumatism or psoriasis), certain eye disorders (e.g. diabetic  
 CC retinopathy, retinopathy of prematurity, neovascular glaucoma,  
 CC retinoblastoma, retrolental fibroplasia, rubeosis), uveitis, macular  
 CC degeneration or graft neovascularization), cancer (e.g. metastatic  
 CC sarcomas or carcinomas), or wound granulation.  
 XX Sequence 704 AA;

Query Match 61.4%; Score 35; DB 22; Length 704;  
 Best Local Similarity 60.0%; Pred. No. 4 le-02;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATD1KGAP 10  
 ||| ||| |||  
 Db 289 catqwkqlq 298

RESULT 4  
 AAR41164  
 Id AAR41164 standard; protein; 977 AA.  
 AC AAR41164;

02-APR-2001 (first entry)

Amino acid sequence of a Tek/tyr fusion protein.

XX Fusion protein, receptor tyrosine kinase, tek, te portion  
 KW immunoglobulin G1, IgG1, and angiogenesis, tumor; ocular neovascularization;  
 KW inflammatory disease; arthritis; rheumatism; psoriasis; eye disorder;  
 KW diabetic retinopathy; retinopathy; neovascular glaucoma; retinoblastoma;  
 KW retrolental fibroplasia; rubeosis; uveitis; macular degeneration;  
 KW graft neovascularization; cancer; metastatic sarcoma; carcinoma;  
 KW wound granulation.  
 CA Synthetic.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FI Peptide 1..18 "signal peptide"  
 FI Protein 19..745  
 FI /note: "tek extracellular domain"  
 FI Protein 746..977  
 FI /note: "pe portion"  
 XX W0200075323-A1.  
 XX 14 DEC-2000.  
 XX 07-JUN-2000; 2000W0-US15706.  
 XX 07-JUN-1999; 990S-0137889.  
 XX (IMMUNEX CORP.  
 XX Corretti DP, Borges LG, Fanslow WC;  
 XX WPI; 2001-112149/12.  
 XX New tek polypeptide antagonist having a fragment of the tek  
 PI extracellular domain, useful for treating mammals with a disease  
 PI mediated by angiogenesis, e.g. tumors, ocular neovascularization or  
 PI inflammatory diseases.  
 XX Claim 41; Page 34-37; 43pp; English.  
 PS The present sequence represents a fusion protein comprising the  
 CC extracellular domain of the human receptor tyrosine kinase and the  
 CC portion of human immunoglobulin (Ig) G1. The tek fragment lacks all  
 CC or part of the region containing fibronectin type III (FNIII) motifs, and  
 CC retains the ability to bind at least one tek ligand. The fusion  
 CC polypeptide is an angiogenesis inhibitor, and a tek antagonist.  
 CC polypeptide of soluble tek multimer, antibodies or antibody fragments are  
 CC useful for treating a mammal having a disease or condition mediated by  
 CC angiogenesis, e.g. a solid tumor, a condition of disease characterized by  
 CC ocular neovascularization. In particular, the tek antagonists are useful  
 CC for treating or preventing inflammatory diseases (e.g. arthritis,  
 CC rheumatism or psoriasis), certain eye disorders (e.g. diabetic  
 CC retinopathy, retinopathy of prematurity, neovascular glaucoma,  
 CC retinoblastoma, retrolental fibroplasia, rubeosis), uveitis, macular  
 CC degeneration or graft neovascularization), cancer (e.g. metastatic  
 CC sarcomas or carcinomas), or wound granulation.  
 XX Sequence 977 AA;

Query Match 61.4%; Score 35; DB 22; Length 977;  
 Best Local Similarity 60.0%; Pred. No. 5 le-02;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATD1KGAP 10  
 ||| ||| |||  
 Db 289 catqwkqlq 298

RESULT 5  
 AAR45440  
 Id AAR45440 standard; protein; 1124 AA.  
 AC AAR45440;

25-JUN-1994 (first entry)

Human orphan receptor kinase.

KW Ork; ligands; antibodies; PCR; amplification.

OS Homo sapiens.

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FH Key Location/Qualifiers
FI 1..18 /note="signal peptide"
FI 746..772 /note="transmembrane region"
FI 211..340 /note="EGF-like repeat"
FI 44 /note="Cys of immunoglobulin domain"
FI 102 /note="Cys of immunoglobulin domain"
FI 19..1124 /note="claimed fragment"
FI 19..745 /note="claimed fragment"
XX
IN W09400469 A
XX
XX 06 JAN 1994
XX
XX 25 JUN 1994; 93WO-US06093.
XX
XX 26 JUN 1992; 92DS-0905600.
XX
XX (IMMUNEX CORP.
XX
XX Ziegler SF;
XX
XX WPI: 1994-026132/03.
XX N-PSDH: AAK55179.
XX
XX DNA and protein sequences for orphan receptor tyrosine kinase -
XX and expression vectors for prodn. of recombinant protein and
XX antibodies specific for the protein, useful in research
XX claim 14; Fig 1; 57pp; English.
XX
XX Degenerate oligonucleotide primers based on the sequence conserved
XX in the kinase domain of all receptor tyrosine kinases were used for
XX PCR of single stranded cDNA from human placental polyA mRNA. PCR
XX prod. BHK 6 contained a novel sequence which was used as a probe to
XX associate longer fragments from a human placental cDNA library. One
XX clone contained the entire coding region and was called the ork gene.
XX the gene prod. shown can be used as a research tool in in vitro assays
XX for detection of ork. Its ligands or their interactions.
XX See also AAK45441.
XX
XX Sequence 1124 AA;
SQ

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Query Match: 61.4%; Score 35; DR 15; Length 1124;  
 Best Local Similarity: 60.0%; Prod. No. 6,400-02;  
 Matches: 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 CATH/KCAEP 10
   III II : I
IB 289 catwkaqlq 298

RESULT 6
AAK73953
ID AAK73953 standard; Protein: 1124 AA.
XX
XX AAK73953;
XX
XX 22 JAN 1996 (first entry)
XX
XX Human TEK tyrosine kinase protein.
XX
XX (Fig 2) receptor tyrosine kinase; DNA primer; cancer; angiogenesis;
XX vasculogenesis; tek.
XX
XX Homo sapiens.

```

Query Match: 61.4%; Score 45; DR 16; Length 1124;  
 Best Local Similarity: 60.0%; Prod. No. 6,400-02;  
 Matches: 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 CATH/KCAEP 10
   III II : I
IB 289 catwkaqlq 298

RESULT 7
AAV40418
ID AAV40418 standard; Protein: 1124 AA.
XX
XX AAV40418;
XX
XX 15 NOV 1999 (first entry)
XX
XX Amino acid sequence of TEK (also known as TEK) protein.
XX
XX TEK protein: HE2 protein; receptor tyrosine kinase; involved in
XX immune response; endothelial cells; tumor associated; vasculature;
XX coagulation; thrombosis; cancer; angiogenesis.
XX
XX Homo sapiens.
XX
XX W09943801-A1.
XX
XX 02-SEP-1999.
XX
XX 26-FEB-1999; 99WO-0300583.
XX
XX 26-FEB-1998; 98GB 004121.
XX
XX (CANCER) CANCER RES. CAMPAIGN TECHNOLOGY.
XX
XX Durrant LG, Hewitt PG, Komaroff JM. Spontaneous
XX
XX WPI: 1999-540580/45.
XX
XX New peptides containing at least one epitope from box receptor
XX tyrosine kinase, used in vaccines against cancer.
XX
XX Disclosures: Fig 1; 60pp; English.
XX
XX The present sequence represents the TEK protein, also known as TEK
XX protein. TEK is a receptor tyrosine kinase. TEK is a member of the

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CC which bind to Bcl-2, the presentation of the epitopes can also stimulate  
CC helper cell and/or cytotoxic T cell responses. The immune response is  
CC directed against endothelial cells in the tumor-associated  
CC vasculature and includes production of antibodies that bind to the  
CC cells, causing coagulation and thrombosis. The immune response is  
CC targeted to endothelial cells lining blood vessels of the tumor (these  
CC cells over-express Bcl-2), so damage to even a few cells will kill many  
CC tumor cells; these target cells are accessible to the immune response  
CC and problems of antigenic heterogeneity, Bcl-2 loss and resistance to  
CC apoptosis (associated with epithelial cells) are unlikely to occur in  
CC normal endothelial cells. TEK epitopes (see AAY6329-24) are used to  
CC generate antithodies, and for prevention and treatment of cancer.  
CC the peptides, and recombinant DNA constructs or viral vectors that  
CC express them, are useful as anticancer vaccines to target endothelial  
CC cells that line blood vessels of the tumor.

XX Sequence 1124 AA;

Query Match 61.4%; Score 35; DB 20; Length 1124;

Best Local Similarity 60.0%; Pred. No. 6,46,02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAIDIKGARC 10

DI III I I I

DE 289 cat42kq1T 298

RESULT 8

AAW88448

ID AAW88448 standard; Protein: 1296 AA.

AC AAW88448;

DE 26-APR-1999 (first entry)

DE Caenorhabditis elegans NPC1 protein orthologue.

XX Niemann-Pick disease type C; NPC1 gene; worm; orthologue;

XX diagnosis; therapy, animal model, cholesterol, neurodegeneration.

XX Caenorhabditis elegans.

XX W09901555-A1.

XX 14 JAN 1999.

XX 02 JUL 1998. 98W00513862.

XX 03-JUL-1997. 97US-0051682.

XX (USSH ) US DEPT HEALTH & HUMAN RESOURCES.

XX Carstee ED, Gu J, Loftus SK, Morris JA, Pavan MJ;

XX Penchev ED, Rosenfeld MA, Tagle DA;

XX WPI: 1999 106056709.

XX N-PSDB: AAW06476-77.

XX New isolated gene, NPC1, is associated with Niemann Pick type C  
XX disease, used to develop products for the study, diagnosis and  
XX therapy of the disease

XX Disclosure: Page 91-95; 10pp; English.

XX This polypeptide comprises the Caenorhabditis elegans orthologue

XX of the human NPC1 polypeptide that is associated with

XX Niemann Pick disease type 2 (NP-C). The polypeptide shows

XX extensive identity (90%) and similarity (58%) to the human

XX NPC1 protein (see AAW88445). Biochemical and genetic analysis of

XX yeast, worm and murine NPC1 model systems will provide resources

XX for understanding the role of NPC1 in intracellular cholesterol

XX homeostasis and in the aetiology of neurodegeneration in NP-C.

CC Release. The provision of the human NPC1 gene sequence (see  
CC AAY062973) enables methods of detecting the presence of mutations in  
CC the NPC1 gene, and thereby facilitates the determination of  
CC whether an individual is an NP-C sufferer or carrier.

XX Sequence 1296 AA;

Query Match 60.5%; Score 34; DB 20; Length 1296;

Best Local Similarity 58.8%; Pred. No. 8,96,02;

Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 0;

QY 1 CAI--DIKGAEC 10

DI I I I I I I

DE 1096 cat434kkaac 1018

RESULT 9

AAW83764

ID AAW83764 standard; peptide: 9 AA.

XX AAW83764;

XX 18-MAR-1996 (first entry)

XX NPC derived structural analog (28-36) binds neurotrophin receptor.

XX Neurotrophin receptor; structural analog; nerve growth factor; beta turn;

XX reverse turn; cyclic; tracer, uncharged; hydrophobic; inhibition;

XX neurite outgrowth; central nervous system; peripheral nervous system;

XX tumour; neuroma; hormone-receptor interaction site; immunisation;

XX receptor domain-function correlation.

XX Synthetic.

XX W09521193-A1.

XX 10-AUG-1995.

XX 07-FEB-1995. 95W0-CA000059.

XX 07-FEB-1994. 943H-0002331.

XX (USMC-) ONIV MCGILL.

XX Cuello AC, Lesautour L, Saratovi DH;

XX WPI: 1995-282741/37.

XX New cyclic peptide(s) which bind to neurotrophin receptor and mimic  
XX or inhibit neurotrophin activity (usual e.g. for inhibiting  
XX neurite outgrowth or treating nervous system disease), tumours, etc.

XX Claim 9; Page 42; 42pp; English.

XX The peptides AAW83760-83 are examples of peptides that bind to the  
XX neurotrophin receptor under physiological conditions in vivo or in  
XX vitro. The peptides are structural analogs of nerve growth factor (NGF)  
XX and contain at least one beta turn (from residue 28 to 43, 44 to 51, or  
XX or 3 consecutive reverse turns (from residue 56 to 65). The peptides may be  
XX linked by one or 2 or 3 or other conjugation procedures and may be  
XX linked to a tracer e.g. a metal chelate or radioactive. The peptides  
XX may contain uncharged or hydrophobic amino acids at the N and  
XX C-termini, which are optionally protected by an fluorenyl protecting  
XX group. The peptides are useful for inhibition of neurotrophin, esp. for  
XX inhibiting neurite outgrowth, treating central or peripheral nervous  
XX system disease, tumours and neuromas, for mapping ligand-receptor  
XX interaction sites and receptor domain-function correlation and for  
XX immunisation. This peptide is derived from residues 28-36 and is  
XX linear.

XX Sequence 9 AA;

XX SQ



KW neurotrophin; NT; p75NGFR; receptor; transmembrane glycoprotein;  
 KW rat; mouse; human; bovine; guinea pig; chicken;  
 KW xenopus; snake; mutant; modification.  
 XX W09418066-A.  
 XX 16 SEP 1993.  
 XX 08 MAR 1994; 94WO-SF00201.  
 XX 06 MAR 1992; 92US-0847369.  
 XX (MOLL/) MOLINER C F I.  
 XX (PERSSON) PERSSON H B.  
 XX Persson HB, Moliner CFI;  
 XX WPI: 1993-303406/38.  
 XX New mutant forms of neurotrophic factor of increased stability -  
 PT have specific positively charged aminoacid(s) replaced, showing  
 PT more selective binding but equiv. biological activity  
 XX Disclosure: Fig 1. 70pp; English.  
 XX Comparison of NCF genes from different species has revealed clusters  
 CC of amino acid residues which are highly conserved across different  
 CC qps. of vertebrates (rat, mouse, human, bovine, guinea pig and chicken  
 CC NCF; AAR41747; xenopus NCF; AAR41748; snake NCF; AAR41749; rat BDNF;  
 CC AAR41750; rat NT 4; AAR41751; and xenopus NT 4; AAR41752).  
 CC New mutant neurotrophic factor (NF) comprises a wild-type NF having,  
 CC as modification, replacement of one or more positively charged amino  
 CC acids, in the amino acid regions 34 or 34-46, with uncharged or  
 CC negatively charged amino acids, so that the mutants have reduced  
 CC ability to bind to p75NGFR (a transmembrane glycoprotein which binds  
 CC NCF with low affinity), c.f. wild-type NF.  
 CC The wild-type NF is pref. NCF, BDNF, NT 3 or NT 4. In the 34-46  
 CC region, the modifications are pref. at Lys2 (or Arg2 in NT)  
 CC Lys2, for NT 3, Arg2, His34, Asn33 and/or Asn91, for BDNF, Lys35,  
 CC Lys96 and/or Arg97, and for NT 4 Glu94 and Arg96 are replaced.  
 CC The mutants differ from wild-type NF as regards receptor binding  
 CC affinity and specificity, esp. they can bind to trk receptor but not  
 CC to p75NGFR. Modifications in the 25-36 amino acid region improve  
 CC stability.  
 XX Sequence 12 AA;  
 SQ  
 Query Match 59.6%; Score 34; DB 14; Length 12;  
 Best Local Similarity 87.5%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 1; Gaps 0;  
 QY 2 ATDIKGA 9  
 IV 111111  
 IV 4 aridike 11  
 RESULT 14  
 AAR41748  
 ID AAR41748 standard; peptide: 12 AA.  
 XX AAR41748;  
 XX 18-MAR-1994 (first entry)  
 DE Conserved NCF region 25-36 (xenopus).  
 XX Nerve growth factor; NCF; brain-derived neurotrophic factor; BDNF;  
 KW neurotrophin; NT; p75NGFR; receptor; transmembrane glycoprotein;  
 KW rat; mouse; human; bovine; guinea pig; chicken;  
 KW xenopus; snake; mutant; modification.  
 XX

PN W09318066-A.  
 XX 16 SEP 1993.  
 XX 08-MAR-1993; 94WO-SF00201.  
 XX 06-MAR-1992; 92US-0847369.  
 XX (MOLL/) MOLINER C F I.  
 XX (PERSSON) PERSSON H B.  
 XX Persson HB, Moliner CFI;  
 XX WPI: 1993-303406/38.  
 XX New mutant forms of neurotrophic factor of increased stability -  
 PT have specific positively charged aminoacid(s) replaced, showing  
 PT more selective binding but equiv. biological activity  
 XX Disclosure: Fig 1. 70pp; English.  
 XX Comparison of NCF genes from different species has revealed clusters  
 CC of amino acid residues which are highly conserved across different  
 CC qps. of vertebrates (rat, mouse, human, bovine, guinea pig and chicken  
 CC NCF; AAR41747; xenopus NCF; AAR41748; snake NCF; AAR41749; rat BDNF;  
 CC AAR41750; rat NT 4; AAR41751; and xenopus NT 4; AAR41752).  
 CC New mutant neurotrophic factor (NF) comprises a wild-type NF having,  
 CC as modification, replacement of one or more positively charged amino  
 CC acids, in the amino acid regions 34 or 34-46, with uncharged or  
 CC negatively charged amino acids, so that the mutants have reduced  
 CC ability to bind to p75NGFR (a transmembrane glycoprotein which binds  
 CC NCF with low affinity), c.f. wild-type NF.  
 CC The wild-type NF is pref. NCF, BDNF, NT 3 or NT 4. In the 34-46  
 CC region, the modifications are pref. at Lys2 (or Arg2 in NT)  
 CC Lys2, for NT 3, Arg2, His34, Asn33 and/or Asn91, for BDNF, Lys35,  
 CC Lys96 and/or Arg97, and for NT 4 Glu94 and Arg96 are replaced.  
 CC The mutants differ from wild-type NF as regards receptor binding  
 CC affinity and specificity, esp. they can bind to trk receptor but not  
 CC to p75NGFR. Modifications in the 25-36 amino acid region improve  
 CC stability.  
 XX Sequence 12 AA;  
 SQ  
 Query Match 59.6%; Score 34; DB 14; Length 12;  
 Best Local Similarity 87.5%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 1; Gaps 0;  
 QY 2 ATDIKGA 9  
 IV 111111  
 IV 4 aridike 11  
 RESULT 14  
 AAR07158  
 ID AAR07158 standard; protein: 13 AA.  
 XX AAR07158;  
 XX 24-JAN-1991 (first entry)  
 DE Nerve growth factor (NCF) peptide fragment.  
 XX Nervous disorders; Alzheimer's disease; Parkinson's disease; stroke.  
 XX Homo sapiens.  
 XX W09010644-A.  
 XX 20-SEP-1990.  
 XX 08-MAR-1990; 93WO-0000149.  
 XX

XX 14-MAR-1989, 89SE-0000899.  
 XX (LOPE-) LOPE MED AB.  
 XX Olson L, Persson H, Ebendal T;  
 XX WP1: 1990-304983/40  
 XX New peptide fragments of nerve growth factor or its precursor  
 XX used to raise specific antibodies for immunoassay, esp. for brain  
 XX tissue  
 XX Claim 1: Page 14; 24pp; English.  
 XX Peptides are Abs raised to them are useful in detecting the presence  
 XX of NGF and precursors, allowing early diagnosis and treatment of  
 XX nervous disorders esp. Alzheimer's and Parkinson's disease, spinal  
 XX cord injury, stroke etc.  
 XX Peptide corresponds to AAs 23 to 35 of human NGF mature protein.  
 XX Sequence 14 AA;  
 SQ  
 Query Match 59.6%; Score 34; DB 11; Length 14;  
 Best Local Similarity 87.5%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 ATP1KGAE 9  
 DB 6 atdtkgke 14  
 RESULT 15  
 AAR07161  
 ID AAR07161 standard; protein; 14 AA.  
 AC AAR07161;  
 XX 24-JAN-1991 (first entry)  
 XX Synthetic nerve growth factor (NGF) peptide fragment.  
 XX Nervous disorders, Alzheimer's disease, Parkinson's disease, stroke,  
 XX Synthetic.  
 XX OS W09010644-A.  
 XX IN 20-SEP-1990.  
 XX 08-MAR-1990; 90W0-0000149.  
 XX 14-MAR-1989; 89SE-0000899.  
 XX (LOPE-) LOPE MED AB.  
 XX Olson L, Persson H, Ebendal T;  
 XX WP1: 1990-304983/40.  
 XX New peptide fragments of nerve growth factor or its precursor -  
 XX used to raise specific antibodies for immunoassay, esp. for brain  
 XX tissue  
 XX Disclosure: Page 11; 24pp; English.  
 XX Peptides are Abs raised to them are useful in detecting the presence  
 XX of NGF and precursors, allowing early diagnosis and treatment of  
 XX nervous disorders esp. Alzheimer's and Parkinson's disease, spinal  
 XX cord injury, stroke etc.  
 XX Peptide corresponds to AAs 23 to 35 of rat (mouse) chicken/human NGF.  
 XX

SQ Sequence 14 AA;  
 Query Match 59.6%; Score 34; DB 11; Length 14;  
 Best Local Similarity 87.5%; Pred. No. 13;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 ATP1KGAE 9  
 DB 7 atdtkgke 14

Search completed: August 01, 2001, 16:41:24  
 Job time: 27 sec



